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<120> Truncated Reelin Protein and DNA Encoding the Same

<130> PH-1167

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<150> JP 2000-109954

<151> 2000-04-11

<160> 28

<170> PatentIn Ver. 2.0

<210> 1

<211> 2274

<212> DNA

<213> *Xenopus laevis*

<220>

<221> CDS

<222> (157)..(1455)

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<222> (157)..(234)

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<221> misc_feature

<222> (241)..(726)

<223> F-spondin domain

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<221> misc_feature

<222> (847)..(1197)

<223> CR-50 epitope region

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cattctactg tcacgttaac ttccatttt cttcacttta actttgaaga atttaaaaaa 60

aaccattaat tatatatatta tataaatata tatatatatan ctctgtatcc caggctgctt 120

atgaagaaag ctcatthaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174

Met Glu Leu Leu His Thr

1

5

ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222

Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys

10

15

20

ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270

Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe

25

30

35

Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His Arg

155

160

165

gga caa gtt att ttc aag gat gcc ctg gca caa caa ctg tgc gaa caa 702

Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu Gln

170

175

180

gga gct cct act gaa gct ccc ttg cgg cct aat tta gcc gaa att cac 750

Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro Asn Leu Ala Glu Ile His

185

190

195

agt gaa agc atc ctt tta cga gat gat ttt gac tca tat aag ctt cag 798

Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe Asp Ser Tyr Lys Leu Gln

200

205

210

gaa ttg aat cca aat att tgg ctc cag tgc aga aat tgc gaa gtt ggt 846

Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys Arg Asn Cys Glu Val Gly

215

220

225

230

gag cag tgt ggt gca att atg cat ggt ggg gca gtc act ttt tgt gat 894

Glu Gln Cys Gly Ala Ile Met His Gly Gly Ala Val Thr Phe Cys Asp

235

240

245

ccg tat gga cca aga gaa ttg ata act gtt caa atg aac aca act acg 942

Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val Gln Met Asn Thr Thr Thr

250

255

260

gca tct gtt ttg cag ttt tct att ggg tca gga tcg tgc agg ttc agc 990

Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe Ser

265

270

275

tat tca gac cct gga att gtg gtg tca tac aca aag aat aat tca tct 1038

Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr Thr Lys Asn Asn Ser Ser

280

285

290

agt tgg atg cca ttg gag aga att agt gct cct tcc aat gtt agc acc 1086

Ser Trp Met Pro Leu Glu Arg Ile Ser Ala Pro Ser Asn Val Ser Thr

295

300

305

310

atc att cac att att tac cta cct cct gaa gct aaa gga gaa aat gtg 1134

Ile Ile His Ile Ile Tyr Leu Pro Pro Glu Ala Lys Gly Glu Asn Val

315

320

325

aaa ttc cgt tgg agg cag gag aac atg cag gca ggt gat gtg tat gaa 1182

Lys Phe Arg Trp Arg Gln Glu Asn Met Gln Ala Gly Asp Val Tyr Glu

330

335

340

gcc tgc tgg gca ctg gat aac att ttg att atc aat gct gct cat aaa 1230

Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile Ile Asn Ala Ala His Lys

345

350

355

gaa gtc gtg tta gaa gac aat cta gat cca atg gac aca gga aac tgg 1278

Glu Val Val Leu Glu Asp Asn Leu Asp Pro Met Asp Thr Gly Asn Trp

360

365

370

ctt ttt ttc cct ggg gct act gta aag cat acc tgt cag tcg gat gga 1326

Leu Phe Phe Pro Gly Ala Thr Val Lys His Thr Cys Gln Ser Asp Gly

375

380

385

390

tcttgtacct tgcatacat ttgtggctag tttatgggtc aatagacagc catcatacat 2015

tagtcagagt aaatcgagca ttacaaaact caatgagcca tagtgagtgt gacaatcaga 2075

agtgactgtc aagtaaatca accatttgct catacagatg cacatttgaa cagtggattc 2135

ttatccagaa agggccattt ttactatca ctctgggatt taaatgccac ttctaattgg 2195

aacttccagg tcacaaaaat agaatggaca tttaaacatc atggttctca ttaccctaa 2255

taaaactccg gttttttta 2274

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<211> 432

<212> PRT

<213> *Xenopus laevis*

<400> 2

Met Glu Leu Leu His Thr Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu

1

5

10

15

Phe Thr Gly Ile Leu Cys Phe Val Val Ala Arg Gly Val Gly Tyr Tyr

20

25

30

Pro Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu

35

40

45

Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala

Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys
 210 215 220

Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly
 225 230 235 240

Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val
 245 250 255

Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser
 260 265 270

Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr
 275 280 285

Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala
 290 295 300

Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu
 305 310 315 320

Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln
 325 330 335

Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile
 340 345 350

Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro
 355 360 365

Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His

370

375

380

Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser

385

390

395

400

Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu

405

410

415

Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly

420

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<210> 3

<211> 2745

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (283)..(2052)

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<222> (283)..(363)

<220>

<221> misc_feature

<222> (284)..(849)

<223> F-spondin domain

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<222> (970)..(1320)

<223> CR-50 epitope region

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tcggtctccc gctaacttcc cccgcggggc tcggttgccc ggaccgctc ggctcgagcc 180

cgccgcccgc tcgccttccc cgcacgcggc tcctccgtgc cggcgcctcc gaaagtggat 240

gagagagcgc gcggggcgcg cggcgggcacg gagcgcgggc gc atg gag cgc ggc 294

Met Glu Arg Gly

1

tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342

Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala

5

10

15

20

acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390

Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro

25

30

35

265

270

275

agt tac tct gac ccc agc atc act gtg tca tac gcc aag aac aat acc 1158
 Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr

280

285

290

gct gat tgg att cag ctg gag aaa att aga gcc cct tcc aat gtg agc 1206
 Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser
 295 300 305

aca gtc atc cac atc ctg tac ctc ccc gag gaa gcc aaa ggg gag agc 1254
 Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser
 310 315 320

gtg cag ttc cag tgg aaa cag gac agc ctg cga gtg ggt gag gtg tat 1302
 Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr
 325 330 335 340

gag gcc tgc tgg gcc ctg gat aac atc ctg gtc atc aat tca gcc cac 1350
 Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile Asn Ser Ala His
 345 350 355

aga gaa gtc gtt ctg gag gac aac ctc gac ccg gtc gac acg ggc aac 1398
 Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val Asp Thr Gly Asn
 360 365 370

tgg ctc ttc ttc cct gga gca acg gtc aag cat agc tgt cag tca gat 1446
 Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser Cys Gln Ser Asp
 375 380 385

ggg aac tcc att tat ttc cat gga aat gaa ggc agc gag ttc aat ttt 1494
 Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser Glu Phe Asn Phe

390

395

400

gcc acc acc cgg gat gta gat ctt tct aca gag gat att caa gag cag 1542
 Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp Ile Gln Glu Gln

405

410

415

420

tgg tca gaa gaa ttt gag agc cag ccc aca gga tgg gat atc ttg gga 1590
 Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp Asp Ile Leu Gly

425

430

435

gca gta gtt ggt gca gac tgt gga acc gta gaa tca gga cta tca ctg 1638
 Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser Gly Leu Ser Leu

440

445

450

gtg ttc ctc aaa gat gga gag agg aag ctt tgc acc ccc tac atg gat 1686
 Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr Pro Tyr Met Asp

455

460

465

aca act ggt tat ggc aac ctg agg ttc tac ttc gtt atg gga gga atc 1734
 Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val Met Gly Gly Ile

470

475

480

tgt gac cct gga gtc tct cat gaa aac gat atc atc tta tat gca aag 1782
 Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile Leu Tyr Ala Lys

485

490

495

500

tttcattcag ggagcttgat acaagttatc agaggtgttc accatgctgt gtggcagcat 2312

ccccgttct aacagattgc tgggtgaaga tgactgaaga caagattggc ttctgttggc 2372

tggtgacccc ttataatagg tatggaagtc aattagcact tcaagggcta tgacttctct 2432

gctcctcttg cataagtgtt gctcccatcc tctgtaaaga actttgctga cctcacattc 2492

acaggatgaa gtgacagtgt gagacatggt aattgcctag ctatctatca aattcaagag 2552

cacaaacca gtttactgtg tattgtcctt cagacgtagc ttttatggca gtaatccaat 2612

ggcttgccct ctgaaggctg gtcaggcttc agtgagagat gacacattta gtaaaggctc 2672

tagagaaatc ccacattcat cgactcattc aaggatttta gctagaaata aaaagaatca 2732

aaaaaataaa tta 2745

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<212> PRT

<213> Mus musculus

<400> 4

Met Glu Arg Gly Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu

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10

15

Leu Leu Leu Ala Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro

20

25

30

Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu

35

40

45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly

50

55

60

Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser

65

70

75

80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser

85

90

95

Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly

100

105

110

Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser

115

120

125

Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe

130

135

140

Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala

145

150

155

160

Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln

165

170

175

Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His
 180 185 190

Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp
 195 200 205

Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser
 210 215 220

Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala
 225 230 235 240

Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys
 245 250 255

Leu Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly
 260 265 270

Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala
 275 280 285

Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro
 290 295 300

Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala
 305 310 315 320

Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val

335

350

365

380

400

415

430

445

460

480

Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile

485

490

495

Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr

500

505

510

Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile

515

520

525

Asn Pro Glu Leu Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys

530

535

540

Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His

545

550

555

560

Val Leu Pro Val Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser

565

570

575

Ile Asn Leu Gly Cys Gly Thr His Gln Pro Gly Asn Arg

580

585

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<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 7

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<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 8

cagcaacaca taggggacaa

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<210> 9

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 9

ggccacgcgt cgactagtac gaattcatct atagcttttt tttttttttt t

51

<210> 10
<211> 35
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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cagtgtcggtt gcttcccacg tgagtcattt tccca

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<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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cgacaggtac aggatgtgtc aacttcattg ccaca

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<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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tcccacaaca aacctaagtt

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<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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atgtcctcac tggaaagatc

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<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 14

cgggataaca ttcagggtat cact

24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 15

atccatggcg gtaactgtct tcct

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<210> 16

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 16

gtcctgatct acaaacacct gctact

26

<210> 17

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 17

aggtagcaca tggacaaaat cc

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<210> 18

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 18

ctgaagcaaa ccagtcaccg tgggtca

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<210> 19

<211> 25

<212> DNA

<213> Artificial Sequence

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[illegible]

7

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 20

ggccctttct ggataagaat c

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<210> 21

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 21

tcaaccattt gctcatacag atgcaca

27

<210> 22

<223> Description of Artificial Sequence:synthetic DNA

<400> 24

gcggacaaca atatgcaagg

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<210> 25

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 25

ggttggtgac aaactggtcc

20

<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 26

cgcgctcgact agtacgaatt

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 27

ctgattggat tcagctggag

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<210> 28

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

<400> 28

attcagccca cagagaagtc

20